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FORM 1 (cDNA sequence provided):

```
1 ATGGACAGAG TTTATGAAAT TCCTGAGGAG CCAAATGTGG ATCCGGTTTC
51 ATCTCTGGAG GAAGATGTCA TCCGTGGAGC CAACCCCCGA TTTACTTTTC
101 CATTTAGCAT CCTTTTCTCC ACCTTTTTGT ACTGTGGGGA GGCTGCATCT
151 GCTTTGTACA TGGTTAGAAAT CTATCGAAAG AATAGTGAAA CTTACCGGAT
201 GACATACACC TTTTCTTTCT TTATGTTTTT ATCCATTATG GTCCAGTTGA
251 CCCTCATTTT TGTCCACAGA GATCTAGCCA AAGATAAACC GCTATCATT
301 TTTATGCATC TAATCCTCTT GGGACCTGTT ATCAGATGTT TGGAGGCCAT
351 GATTAAGTAC CTCACACTGT GGAAGAAAGA GGAGCAGGAG GAGCCCTATG
401 TCAGCCTCAC CCGAAAGAAG ATGCTAATAG ATGGCGAGGA GGTGCTGATA
451 GAATGGGAGG TGGGCCACTC CATCCGGACC CTGGCTATGC ACCGCAATGC
501 CTACAAACGT ATGTCACAGA TCCAAGCCTT CCTGGGCTCA GTGCCCAGC
551 TGACCTATCA GCTCTATGTG AGCCTGATCT CTGCAGAGGT TCCCCTGGGT
601 AGAGTTGTGC TAATGGTATT TTCCCTGGTA TCTGTCACCT ATGGGGCCAC
651 CCTTTGCAAT ATGTTGGCTA TCCAGATCAA GTACGATGAC TACAAGATTC
701 GCCTTGGGCC ACTAGAAGTC CTCTGCATCA CCATCTGGCG GACATTGGAG
751 ATCACTTCCC GCCTCCTGAT TCTGGTGTCT TTCTCAGCCA CTTTGAAATT
801 GAAGGCTGTG CCCTTCCTAG TGCTCAACTT CCTGATCATC CTCTTTGAGC
851 CCTGGATTAA GTTCTGGAGA AGTGGTGCCC AGATGCCCAA TAACATTGAG
901 AAAAATTCTA GCCGGGTCGG CACTCTGGTG GTCCTGATTT CAGTCACCAT
951 CCTCTATGCT GGCATCAACT TCTCTGTCTG GTCAGCTTTG CAGTTGAGGT
1001 TGGCAGACAG AGATCTCGTC GACAAAGGGC AGAACTGGGG ACATATGGGC
1051 CTGCACTATA GTGTGAGGTT GGTAGAGAAT GTGATCATGG TCTTGGTTTT
1101 TAAGTTCTTT GGAGTGAAAG TGTTACTGAA TTACTGTCAT TCCTTGATTG
1151 CCTTGCAGCT CATTATTGCT TATCTGATTT CCATTGACTT CATGCTCCTT
1201 TTCTTCCAGT ACTTGCATCC ATTGCGCTCA CTCTTCACCC ATAATGTAGT
1251 AGACTACCTC CATTGTGTCT GCTGTCACCA GCACCCTCGG ACCAGGGTTG
1301 AGAACTCAGA GCCACCCTTT GAGACTGAAG CAAGGCAAAG TGTTGTCTGA
(SEQ ID NO:1)
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FEATURES:

Start Codon: 1
Stop Codon: 1348
3'UTR: 1351

FORM 2 (transcript sequence provided):

```
1 ATGAACACAA GACCACAACA TTCAGAAAGA ACCTCGACAA TGGACAGAGT
51 TTATGAAATT CCTGAGGAGC CAAATGTGGA TCCGGTTTCA TCTCTGGAGG
101 AAGATGTCAT CCGTGGAGCC AACCCCCGAT TTACTTTTCC ATTAGCATC
151 CTTTCTCCA CCTTTTGTGTA CTGTGGGGAG GCTGCATCTG CTTGTACAT
201 GGTTAGAATC TATCGAAAGA ATAGTGAAAC TTACTGGATG ACATACACCT
251 TTTCTTTCTT TATGTTTTC TCCATTATGG TCCAGTTGAC CCTATTTTTT
301 GTCCACAGAG ATCTAGCCAA AGATAAACCG CTATCATTAT TTATGCATCT
351 AATCCTCTTG GGACCTGTTA TCAGATGTTT GGAGGCCATG ATTAAGTACC
401 TCACACTGTG GAAGAAAGAG GAGCAGGAGG AGCCCTATGT CAGCCTCACC
451 CGAAAGAAGA TGCTAATAGA TGGCGAGGAG GTGCTGATAG AATGGGAGGT
501 GGGCCACTCC ATCCGGACCC TGGCTATGCA CCGCAATGCC TACAAACGTA
551 TGTCACAGAT CCAAGCCTTC CTGGGCTCAG TGCCCAGCT GACCTATCAG
601 CTCTATGTGA GCCTGATCTC TGCAGAGGTT CCCCTGGGTA GAGTTGTGCT
651 AATGGTATTT TCCCTGGTAT CTGTCACCTA TGGGGCCACC CTTTGCAATA
701 TGTTGGCTAT CCAGATCAAG TACGATGACT ACAAGATTCT CTTGGGCCA
751 CTAGAAGTCC TCTGCATCAC CATCTGGCGG ACATTGGAGA TCACTTCCCG
801 CCTCCTGATT CTGGTGCTCT TCTCAGCCAC TTTGAAATTG AAGGCTGTGC
851 CCTTCCTAGT GCTCAACTTC CTGATCATCC TCTTTGAGCC CTGGATTAAG
901 TTCTGGAGAA GTGGTGCCCA GATGCCAAT AACATTGAGA AAAACTTCAG
951 CCGGGTCGGC ACTCTGGTGG TCCTGATTTC AGTCACCATC CTCTATGCTG
1001 GCATCAACTT CTCTTGCTGG TCAGCTTTGC AGTTGAGGTT GGCAGACAGA
1051 GATCTCGTCT ACAAGGGGCA GAACTGGGGA CATATGGGCC TGCACTATAG
1101 TGTGAGGTTG GTAGAGAATG TGATCATGGT CTTGGTTTTT AAGTCTTTT
1151 GAGTGAAAGT GTTACTGAAT TACTGTCATT CTTGATTGCT CTTGCAGCTC
1201 ATTATTGCTT ATCTGATTTC CATTGGCTTC ATGCTCCTTT TCTTCCAGTA
```

FIGURE 1A



Application Serial No. 09/768,781
Inventors: Gennady MERKULOV et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...
Attorney Docket No. CL001057CIP

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1251 CTTGCATCCA TTGCGCTCAC TCTTCACCCA TAATGTAGTA GACTACCTCC
1301 ATTGTGTCTG CTGTCACCAG CACCCTCGGA CCAGGGTTGA GAACTCAGAG
1351 CCACCCTTTG AGACTGAAGC AAGGCAAAGT GTTGCTCTGA (SEQ ID NO:4)

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
gi 6502963 gb AAF14527.1 AF155511_1 (AF155511) KX antigen [Mus ...	366	e-100
gi 10835267 ref NP_066569.1 Kell blood group precursor (McLeod...	361	1e-98
gi 2135606 pir I39294 McLeod syndrome-associated protein XK - ...	358	8e-98
gi 3183551 sp P51811 XK_HUMAN MEMBRANE TRANSPORT PROTEIN XK (KX...	358	1e-97
gi 4759330 ref NP_004668.1 Testis-specific XK-related protein ...	76	8e-13

BLAST to dbEST:

	Score	E
gi 1891549 /dataset=dbest /taxon=9606 ...	383	e-104

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|1891549 Germinal center B cells

Expression information from PCR-based tissue screening panels:

Mixed tissue

FIGURE 1B



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Title: ISOLATED HUMAN TRANSPORTER PROTEINS...
Attorney Docket No. CL001057CIP

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FORM 1:

1 MDRVYEIPEE PNVDPVSSLE EDVIRGANPR FTFPFSSILFS TFLYCGEAAS
51 ALYMVRIYRK NSETYRMTYT FSFFMFSSIM VQLTLIFVHR DLAKDKPLSL
101 FMHLILLGPV IRCLEAMIKY LTLWKKEEQE EPYVSLTRKK MLIDGEEVLI
151 EWEVGHSIRT LAMHRNAYKR MSQIQAF LGS VPQLTYQLYV SLISAEVPLG
201 RVVLMVFSLV SVTYGATLCN MLAIQIKYDD YKIRLGPLEV LCITIWRTLE
251 ITSRLILVL FSATLKLKAV PFLVLNFLII LFEPWIKFWR SGAQMPNIE
301 KNFSRVGTLV VLISVTILYA GINFSCWSAL QRLADRD LV DKGQNWGHMG
351 LHYSVRLVEN VIMVLVFKFF GVKVLLNYCH SLIALQLIIA YLISIDFMLL
401 FFQYLHPLRS LFTHNVVDYL HCVCCQHPR TRVENSEPPF ETEARQSVV (SEQ ID NO:2)

FORM 2:

1 MNTRPOHSER TSTMDRVYEI PEEPNDPVVS SLEEDVIRGA NPRFTFPFSI
51 LFSTFLYCGE AASALYMVRI YRKNSETYWM TYTFSFFMFS SIMVQLTLIF
101 VHRDLAKDKP LSLFMHLILL GPVIRCLEAM IKYLT LWKE EQE EPYVSLT
151 RKKMLIDGEE VLEWEVGHS IRTLAMHRNA YKRMSQIQAF LGSVPQLTYQ
201 LYVSLISAEV PLGRVVMVF SLVSVTYGAT LCNMLAIQIK YDDYKIRLGP
251 LEVLCITIWR TLEITSRLII LVLFSATLKL KAVPFLVLNF LIILFEPWIK
301 FWRSGAQPMPN NIEKNFSRVG TLVVLISVTI LYAGINFSCW SALQRLADR
351 DLVDKGQNWG HMGLHYSVRL VENVIMVLVF KFFGVKVLN YCHSLIALQL
401 IIAYLISIGF MLLFFQYLHP LRS LFTHNVV DY LHCVCCHQ HPRTRVENSE
451 PPFETEARQS VV (SEQ ID NO:5)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 2

- 1 302-305 NFSR (SEQ ID NO: 7)
- 2 323-326 NFSC (SEQ ID NO: 8)

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

- 1 59-62 RKNS (SEQ ID NO: 9)
- 2 169-172 KRMS (SEQ ID NO: 10)

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 6

- 1 64-66 TYR
- 2 137-139 TRK
- 3 157-159 SIR
- 4 252-254 TSR
- 5 264-266 TLK
- 6 354-356 SVR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 3

- 1 17-20 SSLE (SEQ ID NO: 11)
- 2 18-21 SLEE (SEQ ID NO: 12)
- 3 431-434 TRVE (SEQ ID NO: 13)

FIGURE 2A



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[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

126-133 KEEQEEPY (SEQ ID NO: 14)

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 4

- 1 215-220 GATLCN (SEQ ID NO: 15)
- 2 321-326 GINFSC (SEQ ID NO: 16)
- 3 343-348 GQNWGH (SEQ ID NO: 17)
- 4 350-355 GLHYSV (SEQ ID NO: 18)

[7] PDOC00029 PS00029 LEUCINE_ZIPPER
Leucine zipper pattern

100-121 LFMHLILLGPVIRCLEAMIKYL (SEQ ID NO: 19)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	36	56	1.443	Certain
2	74	94	2.084	Certain
3	102	122	0.920	Putative
4	181	201	0.811	Putative
5	208	228	1.744	Certain
6	273	293	1.234	Certain
7	312	332	1.785	Certain
8	366	386	0.828	Putative
9	389	409	1.497	Certain

FIGURE 2B



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BLAST Alignment to Top Hit:

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>gi|6502963|gb|AAF14527.1|AF155511_1 (AF155511) KX antigen [Mus
musculus] Length = 446
Score = 366 bits (930), Expect = e-106
Identities = 179/411 (43%), Positives = 265/411 (63%), Gaps = 11/411 (2%)

Query: 33  FPFSILFSTFLYCGEASALYMVRIYRKNSETYRMTYTFSSFFMFSSIMVQLTLFVHRDL 92
FP S++ S FL+ E A+ALY+ YR + T F + +VQ TL+FVHRDL
Sbjct: 3  FPASVIASVFLFVAETAALYLSSTYRSAGDRMWQVLTLLFSLMPCALVQFTLLFVHRDL 62

Query: 93  AKDKPLSLFMHLILLGPVIRCLEAMIKYLTWLKKEEQEPPYVSLTRKKMLI-DGEEVLIE 151
++D+PL+L MHL+ LGP+ RC E Y + ++ EEPYVS+T+K+ + DG +E
Sbjct: 63  SRDRPLALLMHLQLGPLYRCCEVFCIYC---QSDQNEEPYVSITKKRQMPKDGLSEEVE 119

Query: 152 WEVGHSIRTLAMHRNAYKRMSQIQAFGLGSVPQLTYQLYVSLISAEVPLGRVVLMMVFSLSV 211
EVG + L HR+A+ R S IQAFGLS PQLT QLY++++ + GR +M SL+S
Sbjct: 120 KEVGQAEGKLITHRSASFRRASVIQAFGLSAPQLTLQLYITVLEQNITTGRCFIMTSLLS 179

Query: 212 VTYGATLCNMLAIQIKYDDYKIRLGPLEVLCITIWRTLEITSRLILVLFSATLKLKAVP 271
+ YGA CN+LAI+IKYD+Y++++ PL +CI +WR+ EI +R+++LVLF++ LK+ V
Sbjct: 180 IVYGALRCNILAIKIKYDEYEVKVKPLAYVCIFLWRSFEIATRIVIVLVLFTSVLKIWVVA 239

Query: 272 FLVLNFLIILFEPWIKFWRSGAQMPNNIEKNFSRVGTLVVLISVTILYAGINFSCWSALQ 331
+++NF PWI FW SG+ P NIEK SRVGT +VL +T+LYAGIN CWSA+Q
Sbjct: 240 VILVNFFSFFLYPWIVFWCSGSPFENIEKALSRVGTIVLCFLTLTYAGINMFCWSAVQ 299

Query: 332 LRLADRDLVDKGQNWGHMGLHYSVRLVENVIMVLVFKFFGVKVLNLYCHSLIALQLIAY 391
L++ + +L+ K QNW + ++Y R +EN +++L++ FF + + C L+ LQL+I Y
Sbjct: 300 LKIDNPSELISKSNWYRLLIYYMTRFIENSVLLLLWYFFKTDIYMYVCAPLLILQLLIGY 359

Query: 392 LISIDFMLLFFQYLHPLRSLFTHNVVD---YLHCVCCHQHPRTRVENSEP 438
I FML+F+Q+ HP + LF+ +V + L C C R ++SEP
Sbjct: 360 CTGILFMLVFYQFFHPCKKLFSSSVSESFALLRCACWSS---LRRKSSEP 407
(SEQ ID NO:6)
```

ALIGNMENT OF FORM 1 AND FORM 2:

```
>FORM 2
Length = 462 (Length of FORM 1 = 449)
Score = 900 bits (2301), Expect = 0.0
Identities = 447/449 (99%), Positives = 447/449 (99%)

FORM 1: 1 MDRVYEIPEEPNVDPVSSLEEDVIRGANPRFTFPFSILFSTFLYCGEASALYMVRIYRK 60
MDRVYEIPEEPNVDPVSSLEEDVIRGANPRFTFPFSILFSTFLYCGEASALYMVRIYRK
FORM 2: 14 MDRVYEIPEEPNVDPVSSLEEDVIRGANPRFTFPFSILFSTFLYCGEASALYMVRIYRK 73

FORM 1: 61 NSETYRMTYTFSSFFMFSSIMVQLTLFVHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKY 120
NSETY MTYTFSSFFMFSSIMVQLTLFVHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKY
FORM 2: 74 NSETYWMTYTFSSFFMFSSIMVQLTLFVHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKY 133

FORM 1: 121 LTLWKKEEQEPPYVSLTRKKMLIDGEEVLIEWEVGHSIRTLAMHRNAYKRMSQIQAFGLS 180
LTLWKKEEQEPPYVSLTRKKMLIDGEEVLIEWEVGHSIRTLAMHRNAYKRMSQIQAFGLS
FORM 2: 134 LTLWKKEEQEPPYVSLTRKKMLIDGEEVLIEWEVGHSIRTLAMHRNAYKRMSQIQAFGLS 193

FORM 1: 181 VPQLTYQLYVSLISAEVPLGRVVLMMVFSLSVSVTYGATLCNMLAIQIKYDDYKIRLGPLEV 240
VPQLTYQLYVSLISAEVPLGRVVLMMVFSLSVSVTYGATLCNMLAIQIKYDDYKIRLGPLEV
FORM 2: 194 VPQLTYQLYVSLISAEVPLGRVVLMMVFSLSVSVTYGATLCNMLAIQIKYDDYKIRLGPLEV 253

FORM 1: 241 LCITIWRTLEITSRLILVLFSATLKLKAVPFLVLNFLIILFEPWIKFWRSGAQMPNNIE 300
LCITIWRTLEITSRLILVLFSATLKLKAVPFLVLNFLIILFEPWIKFWRSGAQMPNNIE
FORM 2: 254 LCITIWRTLEITSRLILVLFSATLKLKAVPFLVLNFLIILFEPWIKFWRSGAQMPNNIE 313
```

FIGURE 2C



Application Serial No. 09/768,781
Inventors: Gennady MERKULOV et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...
Attorney Docket No. CL001057CIP

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FORM 1: 301 KNFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLDKQNWGHMGLHYSVRLVEN 360
KNFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLDKQNWGHMGLHYSVRLVEN
FORM 2: 314 KNFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLDKQNWGHMGLHYSVRLVEN 373

FORM 1: 361 VIMVLVFKFFGVKVLNLYCHSLIALQLIIAYLISIDFMLLFFQYLHPLRSLFTHNVVDYL 420
VIMVLVFKFFGVKVLNLYCHSLIALQLIIAYLISI FMLLFFQYLHPLRSLFTHNVVDYL
FORM 2: 374 VIMVLVFKFFGVKVLNLYCHSLIALQLIIAYLISIGFMLLFFQYLHPLRSLFTHNVVDYL 433

FORM 1: 421 HVCVCHQHPRTRVENSEPPPFETEARQSVV 449 (SEQ ID NO: 2)
HVCVCHQHPRTRVENSEPPPFETEARQSVV
FORM 2: 434 HVCVCHQHPRTRVENSEPPPFETEARQSVV 462 (Position 14 to 462 of SEQ ID NO:5)

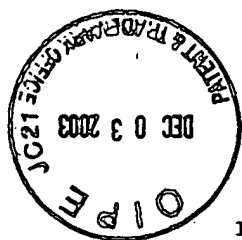
Hammer search results (Pfam):

Model	Description	Score	E-value	N
CE00306	E00306 Membrane_transport_protein_XK	390.8	1.3e-113	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00306	1/1	31	416 ..	1	384 [.	390.8	1.3e-113

FIGURE 2D



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Attorney Docket No. CL001057CIP



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1	TATTATTATT	ATTATTAAGA	CGTAATCTTG	CTCTGTTGCC	CAGGCTGGAG
51	TGCAGTGGCG	TGATCTCAGC	TCACTGCAAC	CTCTGCCGTC	CGGGTTCAAG
101	TTTTTCTCCT	GCCTCAGCCT	CCTGAGTAGC	TGGGATTACA	GTCACGCACC
151	ACCACGACCA	GCTGATTTT	GTATTTT	TAGAGATGGG	GTTTCACCAC
201	GTTGGCCAGG	CTGGTTTCGA	ACTCCTGACC	TCAAGTGATC	TGCCTGCCTC
251	AGCCTCCCAA	AGTGTGGGA	TTACAGGCGT	GAACCACTGT	GCCTGGCCTT
301	CATCTATATT	ATTACCAGGA	GGCAGATGTG	TTCTCTTTT	CTCTGAGGTT
351	TAGAATTATG	CAAATGAAGA	TATGAAAACA	AAAGCTCAGT	GAGGTGGGGA
401	GGATTACACT	TAAGAATACA	GGTAATTTTC	AAAGCTCTTT	AAGACACCCC
451	TCTCAGTTT	TACTAACAGC	TCTCTCTTGG	CTCTTTGCCA	GTCTGTTTAG
501	AATTTGGCAC	CTCTTCATAA	CCTTTCAACC	AAAGACCTGT	AAGTTCATTC
551	TAAAGCTCCT	ATCCTGGCCT	CATTTTGCAA	GTGGAGAAAT	CAAGGCATAA
601	AATATGAGCT	TTTCAGTGTCT	GTGGGCTGAC	CTTGAGTCTT	GACCTTTATC
651	CTGTTCTATC	TTCCCTCCGC	CGAAAACCTCT	GACCTTATTC	CTCCCAGGTT
701	CCCCCTTCAT	GATATTATCT	GGAGGGCAAT	AGGACCTAGG	GAGGTTCCAC
751	CCTGCGGCGG	AGGGAGACAC	ACCTGCCTAA	CAGCGTGGGT	AGAGTGAGTG
801	TTGAAGCAAG	TCACTTAACT	AGTTAGGGAG	GGCGGGGTAG	AAGTGGGGGC
851	CTGCTGCTCC	TAGGGAGGAG	TAAAGCTGTG	GCTCCTGCCT	GGGTCTGGAG
901	GTGGTGGTCA	GAAGTGCTTC	TGAAGAGCGG	CCCAAGCCCC	TTTTTGTCCC
951	GCCACTCCAC	AACGAGCATC	CCTCGGCTGG	CCGCCTGCCC	GGGAACTCTC
1001	CGGCTGGTTT	TGTTTGGCCG	CAGCCGTCCC	GCCCATCTCG	CCCGCCCCCG
1051	CCGTCCCCTG	GCCTTAGTTT	TTGAAGCTGC	CGACCTCTCG	CAGCTGGAAT
1101	CGCAGACCAG	GCAGGACCCT	GGCAGCAGAC	GGCGTCCAAG	AGTTTGGCGA
1151	CCTCCGTCCA	GCCAGGTGG	CGCCCCGCAC	ATCGTGCCCTC	TCACTAGCAA
1201	AGTTTCTCCG	AGGAGAAGCA	CCCCCTCCAG	CCTTTTCTTC	ATCCTGTAGA
1251	GCGAGCGCGC	TCTGCTTCTG	TCCCTCAACA	CTGCATTTCG	AGACAGGGTG
1301	GTGACAATAC	TCCACTCCCG	GGCCAGGCGG	TCTTGGGGGC	GGGGCTTGGG
1351	GGAATCCGAG	GAGCTATCCT	GAGAACCCTG	GA CTGCGCAA	AGGTCCTGAG
1401	AGCGCGCAGG	TGAGCGGGCC	AGCTGATAGC	TACAGCCTAG	CAATAGCTAG
1451	GATACCTAGG	CACTGAACTG	AATCCCCCTCT	TCTGCCCTCC	TTCTTCTGCG
1501	CCCGCTCTTC	TGCCCTGGCT	CAGCTCTCCG	CTGACTTGAG	AGGACACACT
1551	GGTCAGGACT	CTTTGTGAGG	AGCTGCTGAG	TGTGCGTGCC	CCCGACAGAT
1601	CGGCTACACC	CTGCCTGAGG	GGCTGCGAAA	GGAGCCGCCA	CGGAAGCCGC
1651	TGTTCTCATG	ACTCTTCACG	TCCCTGGAGT	TGGACTCTGG	ATGGGGCGCT
1701	GGGATGCTTG	CTTTTGTCTT	GTTCAAGTTT	CACAGCAAGT	ATGTTGACGA
1751	TTGGAATCGG	GGCCAATCAA	GAGTCAAGTT	CAAAGTGGTA	CTCCTGGGCT
1801	TTCCATCCCA	GACTCCAAGT	CGAATCTGAG	TCTAGAAGAG	AGCGGTTTCT
1851	TGCTCTAACT	AGTGAATCTC	TGTTCCCAAA	CTGGACTTGA	CAGAGCTCTC
1901	CTCAGCTATA	CTTGACTGT	AGCGGCCATA	GGGTTCTCTT	GGGGATGGGT
1951	GGGAGGGTGC	TATGAACACA	AGACCACAAC	ATTGAGAAAG	AACCTCGACA
2001	ATGGACAGAG	TTTATGAAAT	TCCTGAGGAG	CCAAATGTGG	ATCCGGTTTC
2051	ATCTCTGGAG	GAAGATGTCA	TCCGTGGAGC	CAACCCCGA	TTTACTTTTC
2101	CATTTAGCAT	CCTTTTCTCC	ACCTTTTGT	ACTGTGGGGA	GGCTGCATCT
2151	GCTTTGTACA	TGGTTAGAAT	CTATCGAAAG	AATAGTGAAA	CTTACTGGAT
2201	GACATACACC	TTTTCTTTCT	TTATGTTTTT	ATCCATTATG	GTCCAGTTGA
2251	CCCTCATTTT	TGTCACAGA	GATCTAGCCA	AAGATAAAC	GCTATCATTA
2301	TTTATGCATC	TAATCCTCTT	GGGACCTGTT	ATCAGGTGAG	CAACTTTTAA
2351	ATCTTTTCTT	TACCCCTTA	ACCCACCCC	AGACTTGGGC	AGAGAAAGAT
2401	GAAAGATTTA	CAAGATGGAT	ACTATGGCTC	TAATCAATTC	TCTCATTTCC
2451	TCCCACTCTC	GGCTTCCCTG	TCTACCATT	AGAAAACCTA	CCTGAAATCT
2501	TAAATGCCAC	CATGATGAAC	ATGTGGTATG	TACTTGTGTT	CCAAAACAAT
2551	GAACGATGCT	ATTTGGGCTG	TGTAAACTAG	AATGGGAACA	ACAAGACGTG
2601	ATCACCTGT	GCATGAAGGC	CATAGCTGCA	GAGTGTGTAA	TTTTATTAA
2651	AAAAATTTTT	TTTTCTGAGA	CAAGGTCTTG	CTCTGCCTCC	CAGGCTACAG
2701	TGCAGTGGTG	CGATCATGGC	TCACTGCAGC	CTTGATCTCC	TGGGATCAAG
2751	CGAACCTCCC	ACCTCAGCCT	CCAAGTAGCT	GGGACCAAAG	GAATGTGTCA
2801	CCATGCCTGG	TTAATTAAAA	AAAAATTTTT	ATAGGCCGGG	TGTGGTGGCT
2851	CATGCCTGTA	ATCCCAGCAC	TTTGGGAGGC	TGAGGCCGGT	GGATCACCTG
2901	AGGTGAGGAG	TTCAAGACCA	GCTGGCCAAC	ATGGTGAAAC	CCCTGTCTCT
2951	ACTAAAAATC	AGCTGGGTGT	GGTGGCGCAT	ATCTGTAATC	CCAGCTACTC
3001	TGGTGGCTGA	GGCAGGAGAA	TCACTTGAAC	CCGGAAGGTA	GAGGTTGCAG

FIGURE 3A



Application Serial No. 09/768,781
Inventors: Gennady MERKULOV et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...
Attorney Docket No. CL001057CIP

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3051 TGAGCCAAGA TCGGTGCCAC TGCCTCCAG CCTGGGCGAT AGAGTGAGAC
3101 TCCATCTCAA AAAAAAAAAA ATTTTTTTTG TAGAGACGGG ATCTCGTTAT
3151 GTAGACTGGG CTCAAGTGAT CTTCTGCCT CAGCCTCCA AAGTGAGCCA
3201 CCACGCCTGG TCTGAGTGT TAATTTTGAC TCTACCTTT TGGATGCTTT
3251 GTAAATTGGA TAAAGTTTC TTTACCCTGA GCTGCTGGG CTGGTGCTAC
3301 TGCCATTTTC AAATTTTCCA GAGTAATGT ACATCTGGAA ACTATTTTAA
3351 ACCATCTGTG GTAATCTGTA CCCCACCCA ATATAGTTCA GTTCTCTGTC
3401 GGTTTATCAG TTTCTATTT ATCTCTTTGT ATATTTCTGC AATAAAGATA
3451 CGAAGTTGGG AGGGGGCAAA GGAAGGCAGT TCATCTCTCT ATGTGGATGC
3501 AGTAGCACAA TTTAATAGTA TCAAGTATT CCATTCAGAT TGCCTTGAAG
3551 TGGAAAGAAT GCACTTAATC CTAGCGAGAT AGGCACCTGT GTCAACAGTC
3601 TCATCTGGAT GCTATGGGGT TTTCAAGTA GAGAGATGTT GCAAACTTA
3651 TGAGTTTCAG AGTAAGGAAT GGACCAAGTT TGTCTTGATT GCGAGAGAGG
3701 CAGACAACCT CAGTCAGCCG AGGAATATGG GTCAGAGTGT TGCAATGGGA
3751 AGATACCTCA TCATTAGACA ACTAAAAAGT CTGTGAAACT AATTAAGGAT
3801 GGAACCTACT CCTTTATAAA ATTTTCATAT TGTACACATG TATAATTTT
3851 ATTTGTCACT TATACCTCAA TAAGGCCAAA AAAATTTTTT ATCAATAAAT
3901 TTTTAAGTGG GGAGGAATCG ATTAGGCTCT ATCAGAGAGA ATATGGGATA
3951 TCAATGGAAA CAGTGGCCTG AAATTTGGAG TCTAGTCTTC GCCTGTCTAT
4001 TGACTGGTTG TGTGTTCTTG GTAAAATCTC TGAAGATGGC TTCACAGGAA
4051 GGCATATAGA GTTCCCTCAT CTGTAAAGCA AATGGGTTAG TCTAAATCAT
4101 GGGTCTCAAA CTCAAACACT TGCAGGGACC AGGCAGGTAT CATAAATGAA
4151 TGAAGCAGGC CTAGTATAAG AAAAAACAGT AGCCTTGTGT GAGATGATAA
4201 ATGGAACAA AGTCTCAGAG AAATACTGAG GAGTAGTGAG TACCATGGTA
4251 ATCTGAAATC TTCATGACCT GCCTGAAGGA GGTAGCCCCT CTAGAGCCCCT
4301 GGCGCATTTG TTCCATGTTG GAATTCAGAC CCAGTATTGT CAGATCCACT
4351 AACTTTTCGG GAGATGCTCC CAAGACAGGA TTTTATATG AAATGTCATG
4401 ATTTTAAATT TTCACAGCTG ACTAAAACAA TAACAACAAC AACACAGGAT
4451 GGACCAAACC ATATCTGTTG GTCAGATATA ACTCAGCTGG CCTATATGCA
4501 TCTTTGGACT GGGTGATGTA AAGGTCCTTT ACGGTTCTAA ATCTTTGAAG
4551 TTAAGCTGTA AAAGGAAGAC CTCATCTTGA CCTTGAAACC AAGAAATTTA
4601 AAGTTGTGAC TACAGGAGCA AATAAACCAT TCATCCCTCC TTTTCAAAT
4651 ACAATATATT GAGTTAACCA ATCGAAAACCT CTCAAGATAA AAATTTCAGA
4701 AAGTACCCAG CTGCACCTCT CCCTCTTTT GACTTCCTTT GTTTGCTTTG
4751 TGAACCTCT GTGTAGAGTG TTGAGTACTG TTTTTCATTT TTGTTGTTTA
4801 GCTTCCACTA GAAATGATTG GGAAGCATT ATAACCTCAG GCAGCTTAGC
4851 CCACAGCAGA GAAAAGATAA AAATCATATA ATTATACTCT GGATTCGCTT
4901 ATTTTCAAGG CCAATTACTT GTTAGATAGG TAGGAAGTGT ATTAGTGTTA
4951 TCAGGCACAT GAAGTGCTT GTAGAGTCTG GGTGCCCTAC ATGAAATGCA
5001 AGCATACTTC CGAAATGAAA ATGTACTCTA ATTTATTGAA GCTTATAAAT
5051 GGACAAACAC CCTTACTTAA ACCAGAAAAT AGCCCTGAGA ATAGAAACAG
5101 AACATTTATG TAAATGTAAA CGGAACATTT CATGCCACCA CCTTCTCCAA
5151 TACTGTTCTC CAATTTAGCA ATAGTACTGA TGGGTTGGGG TTAAATCTA
5201 AAATTTTTC TTTGAAATGC ACTTATGCAG AACAAGAATA GGAAAAAGT
5251 GTTGCTTTTT CTCTCTGTT CTTTCTTTC ATCTTTTCT TTCCAGGTC
5301 TTAGAGTTTG TCCCTAGAAG GTGACAATT CAAACTACAT GCTTCAGAGT
5351 GGTACACATG CATCAGTCTT AGGGTGATCT ATGGAGACTG GCAGCCAGCA
5401 TATGTTCCAA ATTTTCTTAT CAGGAACATA AGGCTAGAGA GCATATCAAC
5451 CTCTGGGCTT GTCTTTGGTC TACTTTTCTG TTAAATTTCA TTGCTGTTAT
5501 TATTATCCTC TCCTCCATA ATTGCTTACC CTGTATTATT TTCTTCTTTC
5551 TTATCTTTTC ATTTACTCAG CAAATATTT TCAAATACCT ACTAAGTGAT
5601 AAGAGCTGTA AACAAGATAA ATACAACCCT TGACCTCAGT CTCTTGGGCA
5651 AGACGTGTTA ATGTCCACTA CAAATGTTCT TACTAGTCAT AAGTAGTCCA
5701 CAGTTTTTAT TCATTAAAGG TGAGTGGCGA AGTGGTAACT CAGGTGTTCC
5751 AGTAACAAGA ATGTTCTAGT TGCTTCTCTT CCACTTACCA CATCAGAACT
5801 GCTAAAGACT TCTGATTTGT ATGGGGGAGG TGGGAGGGGC AGAGCAGGAA
5851 ATGTCATCTT ACCCTTATTC CAAGGATGAT AGGCTTTCAT AAGGATGTTT
5901 TTCTCTTCGT AAAGAAAGAA TCCAGTTTAA AAGGCTTTT TCCACAAACA
5951 GGACAAGAGG CACAAAAAGT AACTATTACA GTGATCTTTC GAGGGCCTAG
6001 TTATGTAGTT CATTACAGTT TGAGTTGTCT TCTTTTAAGT ACTTTTGTG
6051 CTTTGATGGC TTCTGTGTA TATGAGATAT TTTTTCCT CTGATCTGTC
```

FIGURE 3B



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TECH CENTER 1600/2900

6101 CCAAGACTTT TTGGCTGAGA TATGGTTGTG AGCCCTTTCT TGAAAAAGCA
6151 GAATCTGGCC AGGCGCAGTG GCTCATGCCT GTAATCTCAG CACTTTGGGA
6201 AGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCAAGA CCAGCCTGGC
6251 CAACATGGTG AAAACCCGTC TCTACTAAAA ATACAAAAAA AAAAAAACC
6301 TTAGCCGAC ATGGTGGCAC ATGCCGTGTA TCCCAGCTAC TCAGGAGGCT
6351 GAGGCAGGAG AATCGCTTGA ACCCAGGAGG CAGAGGTTAC AGTGAGCTGA
6401 GATCGCGCCA GTGCACTCCA GCCTGGGCGA CAGAGCAAGA CTCTGTCTCA
6451 AAAAAAGAAA AAAAAAGAAA GAAAGAAAAA GAAAAAGCAG AATCTAAAAC
6501 TTTGGTTATG GAGCTGAATG CTTTGAGGGA GGAATGCTTT ACCTACAGAA
6551 TTTGAGGTAA GAAAACAGGG CCTTTGGAAC CTTTATTATT TTGCTAGGAA
6601 AACAGTATCG ACTTAATACC TTTGTGTTCA AGGCACTTT CTACCTGCCA
6651 CAGGCTATT CTTAAAAAGA CAAAACAATT CCTCGAGTCC TCAACAAGT
6701 ACTTCTGAAA CAGTGTCTT AGGTCAGTCG ATGACTGAAC AAAAATGGAT
6751 TTAGATTTCAT GTAACCTGTA GAAGGCATGA TCCACCCCTT GACTTATGAG
6801 AAATGATCAG AACAGAAGAG AGAAAAAGAC AAAAAGTAGT GCAGGCTGGC
6851 CATGGTGTCT CACACGTGTG ATCCCAGCAC TTTAGGATCC CAGCACTTTG
6901 GGTCAAGGCA GTAGGATTGC TTGAGCCCAG GAGTTTGAGA CCAGTCTGGG
6951 CAACATGTCT AGATCTCCTC TCTACACAAA TTAATAATAG CTGGCATGGT
7001 GGCATGCCGC TGTAATCCTA GCTACTCAGA AGGCTGAGGT GGGAGGATCA
7051 TTTGAGCCTA GGAGGTCAAA GCTGCAATGA ATTATGATTG TGCCACTGCA
7101 CTCCAGCCAG GGTGATGGAG TAAGACCTTG TCTCAAAAAT AAAATAAAGT
7151 AGCACAACT CCCCAAGTTA TTTTTTTCCC TCACTACAAC CTCCCTTCCC
7201 AGGACAGCTT AGTTAAGTTT GCATGATGCT TTACTTCTGC AGATGTTTGG
7251 AGGCCATGAT TAAGTACCTC AACTGTGGA AGAAAGAGGA GCAGGAGGAG
7301 CCCTATGTCA GCCTCACCCG AAAGAAGATG CTAATAGATG GCGAGGAGGT
7351 GCTGATAGAA TGGGAGGTGG GCCACTCCAT CCGGACCCTG GCTATGCACC
7401 GCAATGCCTA CAAACGTATG TCACAGATCC AAGCCTTCCT GGGCTCAGTG
7451 CCCAGCTGA CCTATCAGCT CTATGTGAGC CTGATCTCTG CAGAGGTTCC
7501 CCTGGGTAGA GGTGAGTGGG GTCAGGAGAG GGGAGGGCTC CAGTTAAATC
7551 AAGGCTCTTA GAAGTCTAGA CCCAAGCTGT CTAATAAACT GGCCACTAGC
7601 TTCATGTGGC TATTTAACTT AAAATTAAAT AAAATTAAAA ACTTGTTTCA
7651 TAATACTAGC TACATTTCAA GTTCTCAGCA GCCGTGTGTT GCTAGCAACT
7701 ACTGTATTGG ATGGCACAGG TATAAACATT TCCATCATCA CAGAAAGTTC
7751 TATCGGACAG CACTGGGAGA TAGTTAAATA ACTTGTTGAG TCAGACATCT
7801 CAAGCCTGCC AGATTTCTTA AACAGGTAAG CTGTTTAGAC TAAAAATGTC
7851 ACAGATAAAC CTTCTCTGGG CCCAGAAGAA GCTAGTAATA CCAGCAGTCA
7901 GTAGGATATT TTCCCTTGCC CAAAATGTTT AAATTATGCT GTTGTTTGT
7951 TTGTTTAAAG ATGGCAGTCT TTAATAAGAG GTTCCCAAAT AGTACTGATC
8001 ATCAGAAATCA TGTGATGAGC TTCTTTTGA AATTATATTC ACTCCCAGAA
8051 CTTGAATCAA TCTTAATATG TATTTCTAAA AGGTACCCAG TTGATTTTGA
8101 TCAGCCACAT TTGGGAACCA ATGATTTAAT CATTTCTGCT AATGCCAGTG
8151 GAGAGAAAGA AAAGGAGCGT GGGCTGGGCA CGGTGGTTCA AGCCTGTAAT
8201 CCCAGCACTT TGGGAGGCCA AGGCGGGTGG ATCACAAGGT CAGGAGATTG
8251 AGACCATCCT GGCTAACATG ATGAAAACCC GTCTGTACTA AAAATACAAA
8301 AAATTAGCCG GCGTGGTGG CAGGTGCCTG TAGTCCTAGC TACTCGGGAG
8351 GCTGAGGCAG GAGAATGGCG TGAACCTGGG AGGCGGAGCT TGCAGTGAGC
8401 CGAGATCGCG TCACTGCACT CCAGCCTGGG TGACAGAGCA AGACTCCGTC
8451 TCAAAAAAAA AAAAAAAA AAAAAAAA GCGTGGGGTT AATACTAATG
8501 AGAGTCAGGC CTGGACCAAG TTCTGACCTT CACTGTGATC TTTGGAGGAA
8551 GTTACAAAGC AATCACTGAC CTAATTTCCC ACTTGTAAGG GAGGGATCCT
8601 GAAATGAGTA AGACCTTAG CAGAAGATGA AATGTGAGT AGTGTTTCA
8651 AAGTTGAGAT AAATTGTTGT TAATGAATTT TAACAGCCTG AGATTGCTT
8701 CATCTGCTTG GGCAGGCACT GGTATAGGTG TGGGTACAGG TTTGGACCAT
8751 TTCCTATTAG ATTCTAACCC TGTTTGGCAA AGTCCCAGT CTCAAATAAG
8801 GTAAGGAGAA AATTTGCCCT CTTTGTCTT TTTTCCCAC TCAGAAATGT
8851 TCTTGAAGTT CTGTTGTCT TGAAGCTTT CACATACATA GTAGTTTGAG
8901 GAGAAAATC TTTGAAAATG ATGATGCTT TCCTTTAAAT CATCTAATAA
8951 AAATAGGTGT ACATTACGGC TGGGCATGAT GGCTCACGCC TGTAACTCTA
9001 ACACTTTGG AGGCCAAGAC AGGCAGATCA CTTGAAGTTG GGAGTTCAAA
9051 ACCAGCCTGG CCAACATGTT GAAACCCCAT CTCTACTAAA AACACAAAAA
9101 AAATCAAGGA TGGGCATGGT GGCTGATACC TGTAATCCCA GCACCTTGGG

FIGURE 3C



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TECH CENTER 1600/2900

9151 AAGCCGAGGC AGGTGGATCA CCTGAGGTCA GGAGGTTGAG ACCAGCCTGG
9201 CCTGGCGAAA CTCTGTCTCT ACTAAAAATA CAAAAATTAG CCGGGTATGG
9251 TGGTGGATGC TTATAATCCC AGCTACTTGG GAGGCTGATG CATGAGAATC
9301 ACTTGAACCT GGGAGCCGAG ATCTCACCGT TGCACCTCAG CCTGGGCAAC
9351 AGAGCGAGAC TCTGTCTCAA AAAAAAATTC AGCCAGGCGT GGTGGTGGGT
9401 GCCTGTAATC CCAGCTACTT GGGAGGCTGA AGCAGGAGAA TTGCTTGAAC
9451 CTGGGAGGTG GAGGTTGCAG TGAGCTGAGA CTGCACCACT GCACCCAGC
9501 CTGGGCGACA GAGGGAGACT CCCGTCTCAT AAATAAATAA ATAAATAACA
9551 AAAGTAATAC ATGCACAAAA TGACATATAA GTAATTGTAT TTGCACAGAA
9601 AATTTCTGGA AACTATGCAA GAAACTACCT CTGCGGAGTG GGAATGAAAA
9651 GTCAGCAGTC TTACTTTTFA AAATCTTCTT GTATGGTTTG AAAATTTTTT
9701 TTGTGATCAT GCATTACTAG TTTTGGTCTT TATCTTTTTT TAATTACAAA
9751 AGTCAGACAT GATTATAGTA AAAATTAAAA ACCATACAGA ATAGATATAA
9801 AATAGGAAAC GTAATCTCAC TCCCCAAAGA TAACCTCTGT TAATCATCCA
9851 GTATATATCC TTCTGGACTT ATTTTACTA TGTAACATA AACATACATA
9901 CAATATATAT TGTACATGTT TTTGCCCAA AATGGACTGT ATGAAACATT
9951 CTGTCAACAA AGTATTTTTC AAAAGTACAG TATGCCAGTA TGTCTTTTCT
10001 CAAGTTATTT ATATATACAT GTATAACAAT AATAAATAA TAATATACAT
10051 TTCCTTTATA TGAATTAGAC TATTTTATTT CTCCTAATTT TCTATTGATA
10101 GGATTCTATT GATTGTCTCA AAAAGGAAAA AAAAAAGGTAG CACAACCTCC
10151 CCTAGTTATT TTTTCCCTC ATTACAACCT CCCTTCTCAG GACAGCTTTA
10201 GTTAAGTTCC CATGATGCTT TACTTCTGCA GATGTTTGA GGCCATGAGT
10251 AAGGACTTCA CACTGTGGA GAAAGAGGGG CAGCAGGAGC CCTATGTCAG
10301 CCTCACAAAT TTAAATTTT CACAAAAAAG TTGTTTCTA ATTGCAAATT
10351 ATGCCACAGT AAACATCTTT ATAAATACCT GTGTACATGA ATGAGACTTT
10401 GTAGGATAAA TTTATAGCAG TAGAATTGCT GGGTGAAGG ATATGTATGT
10451 TTAAATTTT ATTGATATTG CCAAATAACT CTTCCAAAAA GATATATGAA
10501 TTTATACTCT CACCAACAGT ATACAAATGT GCCTGTTTCT GTTCTTTCAT
10551 ATCTTAAACT CAATATTCTT TATTTGTATA ATTATAAAAT AATTGGCTTT
10601 TAAATAAATT GACTTTTAAA ATAATTCGCT TTCTTTGGTT ATGAATGAAG
10651 CTGAGCATCT TTTTGTGTTT GGTCATTGTG TGTTCTGTGA ATTGCTTGTT
10701 TATATATTTT ACTCGCTTTT TCTAGTGGGT TGTCTTTTTC ATATTAAATT
10751 TTAGGAGCTA TTTACTTATT CTTGTTATTA ATCCTTTTCT TGCTGTGAAT
10801 ATGTATGCAT ATATTTGTAT AATTTTTTGC TTGTACATAC ACACATTTTA
10851 AATATGTATA TACATGTCAT ACGTGTAAATA TGTGTGTGAT ATATTTAATA
10901 TCCACAATAC ACTTTGTAGT ATCTTCTGGC ATTCTGAAGT ATTACATTTT
10951 TATGTATTCA AATTCTTTAT TGCTTTTAGA TTTTGTGCCT TTCTTACAAA
11001 GGCCTATCAC ATCTCTCATC TGGTAGAACA ATTTTCCCCA ATCTTTTAAG
11051 TAGATTAAAT TTCAAGATA TTTTTTAAAT CATCCTACAA AAAACAAAGC
11101 AAAATAATAA CAGCAAAAGA AAAAAACATT TCATTGAGAT TCCGATTGAG
11151 ATTTGCATCA AATTACTTAG GTTATTTTGG GAGAATTTAC ATCTTTATAG
11201 GATTGTTGGA TTTCATATTG TGAAATGATA AATCTCTCCA TTTTATTAAA
11251 TATTTTAAAC TGTAACCTCAG TAAATTTGTA TAGTTTTCTT CAGTAAAGTT
11301 GTATAGTTTT CTGCTATGA GTCTTACATT TTTATAAGGC TTACTTTCAG
11351 ATGTTCTATC AGTTTTAAAA TGACCTGATT TTCTAAGTAG CAGGATAGTA
11401 TCCAGGTAAA GTAAACCCAC CTACCATACT TTTGGAAATA GGGGGATGAT
11451 GAAGATGACA AAGAATAGGA AGAAAGAGGA GGAGGGGGAG GAGGAGAAAA
11501 AGGAAAGGAA GAAGGGAAGA AGGAAGAAGA AGAAAGAAGA ACACAGCTAA
11551 AAGAATTTAC TAGGTTCTAG GCATTTCTCT AAGCCCTTTA CATGTAAATG
11601 TTTATTTAAT CTTTACCACA ACCCTATGAG ATAATTATCA TTCTCATTTT
11651 ACAGACGAAG AAACAGACGC ACTGAGAGTT TAAGTATATT CCCCCAAGGT
11701 CCCATAAGCA AAGATTGGAT TGGAATTCAG GGTGTTTGCC TCCAGAGCCT
11751 GTGTATTTTG TTCTCTTATG GCATGAGTGT ATTTGTAGGG ACACAGATTG
11801 AAAATGTTTT GACATTTATT GGAAGCATCA GGTTTTTTTC CTTCTGTTAC
11851 ACTACTAATC AATAAATGAG TTCTAATGTA AGGGAAAGCA TCGCCACACA
11901 GCTGGATGTA TGCTCTCACA TTCCCAGTTA CATAAGGTGC ATCAGCTCTT
11951 GAGGATGGGA CTGAGAATGG TTGAGAAAGA CAAGAGTCAC CACTTCAAGA
12001 GTCTCCAATT CCAGTCTCTG AGATTCCAAC ACTCTACTTA AAATGAAGA
12051 ACTCAGAGCT GTGCTTCTT TTGGGTTTAC ATGGGGGAAA TCTTAACCTT
12101 TCCTCCACTA AAAGTAAAG ATTAAGTTGA CATCTCTATG GCCACCTTTT
12151 CCCTACATCA AGTGTTTTAA TAGGAACAGA AAACCTCAGC TTTCTTTTGG

FIGURE 3D



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TECH CENTER 1600/2900

12201 GATGAGTATT CCTCAGCCAT CCCACTTCTC TTGAGAGCAC TGGATTTTTC
12251 TTAGTAATCA GCATCCTTTG ACATAAAGGA AGAAAAGGAA AGGGCCACCT
12301 GTGTCATCTA TAGTTGAGGC TTAGGTAGGT TAGGGAGCAT CCTGGCTCTT
12351 TAGGGCCACT ACTCTAACAT ATGGTTCCAT GGATGTCATG GGTGAGGCAA
12401 CAGGGTTTGG AAATTTTGA ACTACTCTGC TGCAAACCTA GAGATTCCTA
12451 ACATATGGGG GTAATGAATT GACATTGCTG ATGACAAATA TAAGCAACTC
12501 TTGAGTATCT CAGTGAATTG AGAACTGAGG TACATAGATA TTCAGTGAAT
12551 TCCAAAAGTT CCCATACAGC TGAACCAAGG ATTTCTTTCT TTCTTTCTTT
12601 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT
12651 TTCTTTCTTT TCTTTCTTTT TTTCTTTCTT TCTTTCTTTT TTTCTTTCTT
12701 CTTTCTTTCT CTTTCTTTCT TTTCTTTCTT CTTTCTTTCT CTTTCTTTCT
12751 TCTCTTTCTT TCTCTCTCTC TCTTTCTGTC TTCTTCCCTT CCTCCCTTTC
12801 TCTCTTTCTT CTTTCTTTCT TTCCCTTCTT CTTTACAGGC ATGCACCACC
12851 ATGCCAGCT AATTTTGTGA TTTTGTAGTAG AGTACCGGT TTCACCATGT
12901 TGGTCAGGCT GGTCTTGAAC TCCTGACCTC AGGTGATCCA CCCACCTCAG
12951 CCCCAGCAAG TGCTTGGGAT TACAGGTGTG AGCCACCGTG TGCACGGCTG
13001 GAACCAAGGA TTTCTAATTA GTTTTATTTT TTATTTTCTT TCTTTTCTGAG
13051 AAGGAGTCTC ACTCTGTCTC CCAGGCTGGA GTGCAGTGGG GCAATCTCAA
13101 CTCACCTCAA CCTCTGCCCT GTGGGTTCAG GTGATTCTCG TGCCCTCAGCC
13151 TCCTGAGCAG CTGGGATTAC AGGCATGCCA TCATGCCTGG CTAATTTTCT
13201 TTTCTTTCTT TTTGAGACAG AGTCTCACTC TGTGCCCCAG GCTGGATCGC
13251 AGTGGTGCAA TCACGGCCCA CTATTACCTC TGCCTCCCAG GTTCAAGTAA
13301 TTCTCCTGCC TCAGCATCCC AGGTAGCTGG GAATACAGGT GCACGCCACC
13351 ACGCCTGACT AATATTGTGA TTTTGTAGCG AGATGGGGTT TCATCATGTT
13401 GGCCAGGCTG GTCTCGAAGT CCTGACTTCA GGTGATCCAT CCGCCTTGGC
13451 CTCCCAATGT CTTGGGATTA CAGGCATGAG TCACCGCGCT CAGCCTAATC
13501 AGGTATTTTA TGCACCTCTC CTAATCTCAG AAGTCTTCAT TAATTCCACA
13551 AACATTTATT GAGCACCTGC TATGTTCCAG GTAATATGTT AGGCTATGGG
13601 AATACAGCAG TGAAGAAAAC ATGGTCCCTC CTGCCTTCAT GGAATTTTCA
13651 ATACACATTT TGACACATCA CTGAAGCTAA GTGTTCTAGA AACACACAAA
13701 CAATGTTAGT TCCTTGAACA AGATATACAT CAAAGAAGGG ACTTCTATTA
13751 GCAAGAGGCT TCTCTATGAG TCTCCTAAGA CTGGATTTT TCAGATAGAG
13801 TTCTTTCCGC GTTATTCAAT GTTTGCTCCG AAGCCTGCTT CATCAGCAAA
13851 GTCTGCCTGA TACCTTTATA TGTACTCTTC TCACGTTAGT GACTTCTCAA
13901 TGTTCTAAGA CCCATGCTTT TTAAGGAAGT TTATTTTGTGA TATTTATATG
13951 ATTATTAAAG TGTTACAGTA TATGTTTCATC ATGAGAAAT TAGAAAATAG
14001 AGAAATGTAG AGAAAAGAT TTCTAAACT GATATAAGAC TATCACACAC
14051 AAAAAAGAT ATTTTGGTTC ATTTTTCAG TTTTGTGTC ATCTATTTTG
14101 TTTTATTGTA TATATTCAAG GTGTACAATG TGATGTTTCG ATGTATGTAT
14151 ACATTGTGAA ATGATTACCA CAACCAAACT AATTAACACA TTCATCACCT
14201 CACATAGTTA TCATTTTGTG ACGTGTGTGT GTGTGTGTGT GTGTGTGTGT
14251 GGTAACCTT AAGATCTACT CTCTTTAAAA ATTTCAAGTA CACAATACAT
14301 TATTGTCAAC TATAGTCATC ATGTTGTACA TTAGAGCTCT GAAACTTATT
14351 TATCTTATAA CTCTAAATTT GTAGCCTTTG ATCAAAATCC TTCTATTTCC
14401 CTAAATCCCC ATCCCCTGGT AACCACCCAT TCTACTCTGT TGCTAGGTGT
14451 TCAACTTTTT TAGATTCCAC ATATAAGTAA GACAATGCAG TATTTTCTT
14501 TATGTGTCTA GCTCATTTCA CTTAGCATAA TGTCCTCTAG GTTCATCTGT
14551 GTTGTACAGG ATGGCAGAGT TTCTGTAATT TTATGGTTGA ATAATATTCA
14601 TACACACACA CACACACAG CACACACACA CACACACACA CAGACACACC
14651 CACCAGATTT TCTTTATCCA TTCATCTGTC AACAGATACT GAGTTTGTGT
14701 CCATATCTTG GCTATTGAGA ATAATACTAC AATGAGCATG AGAGTGCAGA
14751 TATCTCTTTG AGATACTGAT TTCCTTTAGG TATACACCCA GCAGTGGGAT
14801 TATTTGATCG TTTGGCCGTT CTGTTTGTAA TTTTGTGGA GAACCTCCAT
14851 GCTGTTTTCC ATAATGGCTG TGTCAGTTTA TGTTCCACAA AACAGTGTAC
14901 AAGGTCCTTT TTCTTACATC CCCACCAACA CTTTTTTTTT TTAATAATAG
14951 CCATTCTAAC AGGTGTGAGG TGATATCTCA TTGTGGCTTT GATTTGCATT
15001 TTTGTGATGA TTAGTGATGT TGAACACCTT TTCATATACC TGTTGGCCGT
15051 TTGTATACCG CCTTCGGAGA AAGTCTATTC AAGTGCATGC TATTTGTTTA
15101 CATAGCTGTG CATTATTTG CATTTGCTCT TAACTGGAGC TCTCAAGTCT
15151 CACCCGTCAT CTCTCTGGAC CTCTGGGTAA TAAGTACAGC CTTCAATACC
15201 AACATTGACT GATTGCCTGT TTTTGTTTT GTTTTGTGT TTAACAGTTG

FIGURE 3E



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TECH CENTER 1600/2900

15251 TGCTAATGGT ATTTTCCCTG GTATCTGTCA CCTATGGGGC CACCCTTTGC
15301 AATATGTTGG CTATCCAGAT CAAGTACGAT GACTACAAGA TTCGCCTTGG
15351 GCCACTAGAA GTCCTCTGCA TCACCATCTG GCGGACATTG GAGATCACTT
15401 CCCGCCCTCCT GATTCTGGTG CTCTTCTCAG CCACTTTGAA ATTGAAGGCT
15451 GTGCCCTTCC TAGTGCTCAA CTTCTGTATC ATCCTCTTTG AGCCCTGGAT
15501 TAAGTTCTGG AGAAGTGGTG CCCAGATGCC CAATAACATT GAGAAAAACT
15551 TCAGCCGGGT CGGCACTCTG GTGGTCCTGA TTTCAGTCAC CATCCTCTAT
15601 GCTGGCATCA ACTTCTCTTG CTGGTCAGCT TTGCAGTTGA GGTTGGCAGA
15651 CAGAGATCTC GTCGACAAAG GGCAGAACTG GGGACATATG GGCCTGCACT
15701 ATAGTGTGAG GTTGGTAGAG AATGTGATCA TGGTCTTGGT TTTTAAAGTTC
15751 TTTGGAGTGA AAGTGTACT GAATTACTGT CATTCCTTGA TTGCCTTGCA
15801 GCTCATTATT GCTTATCTGA TTTCCATTGG CTTTCATGCTC CTTTCTTCC
15851 AGTACTTGCA TCCATTGCGC TCACTCTTCA CCCATAATGT AGTAGACTAC
15901 CTCCATTGTG TCTGCTGTCA CCAGCACCCCT CGGACCAGGG TTGAGAACTC
15951 AGAGCCACCC TTTGAGACTG AAGCAAGGCA AAGTGTGTGTC TGATTCTATT
16001 TTCTGGGTAT TTTAGGAAGA GTTGGGAGTT GCCAAGAGTA ACCATGAAAT
16051 TGAACGAAAG GATGAGGTTT ATGGGTGAGA TACCCATCAG TACATTTTCT
16101 TGACTTTTCT GTTAAGCCTA TCAGAAGAAA GAGCAACTCC CAAATAGGTT
16151 TTATTTTCTT AAGAGTTACC ACTATGTTTG GAAACAGGGG GTATCGACTA
16201 TATAGTTGAA AGGGTCAGAA ATACCATTCA CACCCTTCTT ACCCAAGTCA
16251 ATTGGAATAA CTTGTCTTCA AACACTTTAG GCTCTCTAAA GTGACCTTCT
16301 AGCTCTGCTC ATTTGCTTGA TGCATTTCTG AGCTTTCCTG GGCTGAGCTG
16351 AAGGCCCAGA ATCCCGCTAG AATATATCCT GACTGATCAG AGGATATGAC
16401 AGCTTACCAG CTAAGAGTAC CTCCCAGGAA ACAGTCTGAC TAATGTGGAA
16451 CCTGCAACTG TCAGTGTGGC TGGGGTCTTT TTAATTCCAG TGAGAAGCTC
16501 TGGCTGAGAA GAAAATCACC ACTATTAAAA AAGCTGCTCC CCAAGCAGAT
16551 TAGCTCTCTG TTAGGATTTT ACTAGTGGCC ATTCAGCAAG GACCTCTCTT
16601 TACAGTGGCA CTTCATAGGC ACACTCTAAG GAGAAAGTGC AGAGTAGAAT
16651 TCCTTCAGGG CATAAGCCAA AATGACTCTT TTTCTCAGGG ACCTGCATGG
16701 GCCTCCAGCT TGTCTATTGG AATTGTTAAG TGAAGCCTCT CACTTAGTGC
16751 CTCATTAGCA GAGATTTCTT CCAACCCAGC TTTTCTGTGC TCTTGGTATT
16801 TTACTIONTGT ATGTGGACCT CAGAGAAGCT GAAGTGTAAAT TGAAAATGTT
16851 TCCGATGTGT GGAAGAAATG AAGACTGCTT TGTGTCTGCT GTTGTCTTGA
16901 GTATTTTCAAT AATGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTATGTG
16951 TATGTGTGTA GGGAAGAAAG TAATAATGGC TGAGACATCA CCTTCATGTT
17001 GTTTGCGATT GGGATGGGTG ACTAACACTC CAAGGTAGAG TGAAGGCAGA
17051 GGAGGGAAAC AAGATCACAT TAAATCATCA TCAGTACTGG TTTCTGCCCTA
17101 CAGGAGTTTA CTTTTTTTTT TTTTCTTTT TTGAGATGGA GTCTCGCTCT
17151 GTTTTCTAGG CTGAAGTGCA GTGGTGTGAT CTTGGCTCAC TGCAGCCTCT
17201 GCCTCCTGGG TTCAAGCAGN NNNNNNNNNN NNNNNNNNNN NNNNAGTGAT
17251 CCACCCGCCT CGGTCTCCCA AAGCACTGGG ATTACAGGCA TGAGCCACCT
17301 CACGCGGCCA GGATTTTACT TTATAACAAG GAACATATGT TTATCAACCC
17351 TCTGTTCTGT CCTATACCCC CAGTGGACGA ATGCATGTCT CCTTTTCTCC
17401 TATATCTCAA TGTTTACATC TCATATCAGT TGGGTATTTT GATAGGAATG
17451 TCAGCCAGCT ACCTCTGAGG TAACCAAGGG ATTGAAGTTA CTATGGCCAC
17501 TGCCTATTGG GACCAAATAT CCCAGCATTT ACCTAACTAA TGCTTGCCCC
17551 TCACAGACCA GGAAAATTAA AAGAACTCCT AGTCGTGGCC ACCACAACAC
17601 TTCAAGAAAT TGTGAACAAT CTGACCTAGG GCTTCCTGTC CTCATCCAAT
17651 TTTACTCTTG GTAGCATGCT AAGAATTAT CTTTAGTCAT TTCCTCTCCT
17701 CTTATCCAAT GTCAGGACAT TATGTTGAGG GAGTCTCTC TTCTAAGTAG
17751 CAGGCTGTT AACCAAAGTA TCTTATTTCT TGGCATGGCT AGCATGGTTT
17801 TCCCTTCACT AGCCACTGTT TGGGACTAAA AGGATTATAT ACTTAATTGT
17851 GGAGAGACTG TATGGAAGT CTTTGGAAAC GTGGAGAGCT CCTTTCTTCA
17901 ACCCAACTC CCCCATTTCA TTTTTCATGA TGAAGAGACT TAGTTATTGT
17951 CATATAAAGC TCACCTGCTG TCTTCTAACT ATGTTATTCA AGG (SEQ ID NO:3)

FEATURES:

Gene Structure

FORM 1:

Start: 2001
Exon: 2001-2335

FIGURE 3F



Intron: 2336-7242
Exon: 7243-7511
Intron: 7512-15247
Exon: 15248-15990
Stop: 15991

FORM 2:

Start: 1962
Exon: 1962-2335
Intron: 2336-7242
Exon: 7243-7511
Intron: 7512-15247
Exon: 15248-15993
Stop: 15991

CHROMOSOME MAP POSITION:

Chromosome 23

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
2584	G	C	Intron
2655	A	T	Intron
3693	G	A	Intron
3992	G	C	Intron
6285	-	A	Intron
7066	A	T	Intron
14223	-	T G	Intron
16915	-	G T	Beyond ORF (3')

Context:

DNA

Position

2584 ATAAACCGCTATCATTATTTATGCATCTAATCCTCTTGGGACCTGTTATCAGGTGAGCAA
CTTTTAAATCTTTTCCTTACCCCCCTAACCCACCCAGACTTGGGCAGAGAAAGATGAA
AGATTACAAGATGGATACTATGGCTCTAATCAATTCTCTCATTTCCTCCCACTCTCGGC
TTCCCTGTCTACCATTCAGAAAACCTTACCTGAAATCTTAAATGCCACCATGATGAACATG
TGGTATGTACTTGTGTTCCAAAACAATGAACGATGCTATTTGGGCTGTGTAACTAGAAT
[G, C]
GGAACAACAAGACGTGATCACCTGTGCATGAAGGCCATAGCTGCAGAGTGTGTAATTTT
ATTTAAAAAATTTTCTGAGACAAGGTCTTGCTCTGCCTCCAGGCTACAGTGCA
GTGGTGCGATCATGGCTCACTGCAGCCTTGATCTCCTGGGATCAAGCGAACCTCCACCT
CAGCCTCCAAGTAGCTGGGACCAAGGAATGTGTACCATGCCTGGTTAATTAAAAAAA
ATTTTATAGGCCGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAGGCTGAG
(SEQ ID NO: 20)

2655 TTTTCCTTACCCCCCTAACCCACCCAGACTTGGGCAGAGAAAGATGAAAGATTTACAAG
ATGGATACTATGGCTCTAATCAATTCTCTCATTTCCTCCCACTCTCGGCTTCCCTGTCTA
CCATTAGAAAACCTTACCTGAAATCTTAAATGCCACCATGATGAACATGTGGTATGTACT
TGTGTTCCAAAACAATGAACGATGCTATTTGGGCTGTGTAACTAGAATGGGAACAACAA
GACGTGATCACCTGTGCATGAAGGCCATAGCTGCAGAGTGTGTAATTTTATTTAAAAAA
[A, T]
TTTTTTTTTCTGAGACAAGGTCTTGCTCTGCCTCCAGGCTACAGTGCAAGTGGTGCGATC
ATGGCTCACTGCAGCCTTGATCTCCTGGGATCAAGCGAACCTCCACCTCAGCCTCCAAG
TAGCTGGGACCAAGGAATGTGTACCATGCCTGGTTAATTAAAAAAAATTTTATAGG
CCGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAGGCTGAGGCGGTGGATC
ACCTGAGGTCAAGGATTCAGACCAAGCTGGCCAACATGGTGAAACCCCTGTCTCTACTAA
(SEQ ID NO: 21)

FIGURE 3G

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3693 TCTCTGTCGGTTTATCAGTTTCCTATTTATCTCTTTGTATATTTCTGCAATAAAGATACG
AAGTTGGGAGGGGGCAAAGGAAGGCAGTTCATCTCTCTATGTGGATGCAGTAGCACAAAT
TAATAGTATCAAGTATTTCCATTTCAGATTGCCTTGAAGTGGAAGAATGCACTTAATCCT
AGCGAGATAGGCACCTGTGTCAACAGTCTCATCTGGATGCTATGGGGTTTTCAAGGTAGA
GAGATGTTGCAAACTTATGAGTTCAGGAGTAAGGAATGGACCAAGTTTGTCTTGATTGC
[G,A]
AGAGAGGCAGACAACCTGCAGTCAGCCGAGGAATATGGGTGAGAGTGTGCAATGGGAAGA
TACCTCATCATTAGACAACCTAAAAAGTCTGTGAACTAATTAAGGATGGAACCTACTCCT
TTATAAAATTTTCATATCTGTACACATGTATAATTTTTATTTGTCACTTATACCTCAATAA
GGCCAAAAAATTTTTATCAATAAATTTTTAAGTGGGGAGGAATCGATTAGGCTCTATC
AGAGAGAATATGGGATATCAATGGAAACAGTGGCCTGAAATTTGGAGTCTAGTCTTCCGC
(SEQ ID NO: 22)

3992 CGAGAGAGGCAGACAACCTGCAGTCAGCCGAGGAATATGGGTGAGAGTGTGCAATGGGAA
GATACCTCATCATTAGACAACCTAAAAAGTCTGTGAACTAATTAAGGATGGAACCTACTC
CTTTATAAAATTTTCATATCTGTACACATGTATAATTTTTATTTGTCACTTATACCTCAAT
AAGGCCAAAAAATTTTTATCAATAAATTTTTAAGTGGGGAGGAATCGATTAGGCTCTA
TCAGAGAGAATATGGGATATCAATGGAAACAGTGGCCTGAAATTTGGAGTCTAGTCTTCC
[G,C]
CCTGTCTATTGACTGGTTGTGTGTTCTTGGTAAAATCTCTGAAGATGGCTTCACAGGAAGG
CATATAGAGTTCCCTCATCTGTAAAGCAAATGGGTAGTCTAAATCATGGGTCTCAAACCT
CAAACACTTGCAGGGACCAGGCAGGTATCATAAATGAATGAAGCAGGCCTAGTATAAGAA
AAAACAGTAGCCTTGTGTGAGATGATAAATGGAAACAAAGTCTCAGAGAAATACTGAGGA
GTAGTGAGTACCATGGTAATCTGAAATCTTCATGACCTGCCTGAAGGAGGTAGCCCCCTCT
(SEQ ID NO: 23)

6285 TCTTTTCGAGGGCCTAGTTATGTAGTTCATTGAGTTTGAGTTGTCGTCTTTTAAGTACTT
TTGTTGCTTTGATGGCTTCCTGTGTATATGAGATATTTTTTTCTCTGATCTGTCCCAA
GACTTTTGGCTGAGATATGGTTGTGAGCCCTTTCTTGAAAAAGCAGAATCTGGCCAGGC
GCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAAGCTGAGGTGGTGGATCACCTGA
GGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAAACCCGTCTCTACTAAAAATAC
[-,A]
AAAAAATAAATAACCTTAGCCGGACATGGTGGCACATGCCTGTAATCCCAGCTACTCAGG
AGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCAGAGGTTACAGTGAGCTGAGATCG
CGCCAGTGCCTCCAGCCTGGGCGACAGAGCAAGACTCTGTCTCAAAAAAAAAAAAAAAAAA
AGAAAGAAAGAAAAAGAAAAAGCAGAATCTAAACCTTGGTTATGGAGCTGAATGCTTTG
AGGGAGGAATGCTTTACCTCACGAATTTGAGGTAAGAAAAACAGGGCCTTTGGAACCTTCA
(SEQ ID NO: 24)

7066 TTGTAGAAGGCATGATCCACCCTTTGACTTATGAGAAATGATCAGAACAGAAGAGAGAAA
AAGACAAAAAGTAGTGCAGGCTGGCCATGGTGTCTCACAGTGTGATCCCAGCACTTTAG
GATCCCAGCACTTTGGGTCAAGGCAGTAGGATTGCTTGAGCCAGGAGTTTGAGACCAGT
CTGGGCAACATGTCTAGATCTCCTCTCTACACAAATTAATAAGTGGCATGGTGGCAT
GCGCCTGTAGTCTAGTACTCAGAAGGCTGAGGTGGGAGGATCATTTGAGCCTAGGAGG
[A,T]
CAAAGCTGCAATGAATTATGATTGTGCCACTGCCTCCAGCCAGGGTGATGGAGTAAGAC
CTTGTCTCAAAAATAAATAAAGTAGCACAACCTCCCCAAGTTATTTTTTCCCTCACTA
CAACCTCCCTTCCAGGACAGCTTAGTTAAGTTTGCATGATGCTTTACTTCTGCAGATGT
TTGGAGGCCATGATTAAGTACCTCACACTGTGGAAGAAAGAGGAGCAGGAGGCCCTAT
GTCAGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGGAG
(SEQ ID NO: 25)

14223 AAGGAAGTTTATTTTGTATATTTATATGATTATTAAGTGTTACAGTATATGTTTCATCAT
GAGAAATTTAGAAAATAGAGAAATGTAGAGAAAAAGATTTCTAAACTGATATAAGACTA
TCACACAAAAAAGATATTTTGGTTCATTTTTTCAATTTTTTGTGCATCTATTTTGT
TTATTGTATATATTCAGGTGTACAAATGTGATGTTTCGATGTATGTACACATTGTGAAAT
GATTACCACAACCAACTAATTAACACATTCATCACCTCACATAGTTATCATTTTTGTAC
[-,T,G]
TGT
TCAAGTACACAATACATTATTGTCAACTATAGTCATCATGTTGTACATTAGAGCTCTGAA
ACTTATTTATCTTATAACTCTAAATTTGTAGCCTTTGATCAAAATCCTTCTATTTCCCTA

FIGURE 3H

A circular black ink stamp from the Office of Intellectual Property (OIPE). The text "OIPE" is at the top, "JC21" is at the top right, "DEC 03 2003" is in the center, and "PATENT & TRADEMARK OFFICE" is at the bottom.

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FIGURE 31